

Result No.	Score	Query	Match	Length	DB	ID	Description
1	36	63.5	367	1	INX4_DRONE	Q9YX6_drosophila	Q9YX6 drosophila
2	35	63.6	244	1	PHOS_MOUSE	Q9YX8_mus_musculus	Q9YX8 mus musculus
3	35	63.6	245	1	PHOS_BOVIN	P14632_bos_taurus	P14632 bos taurus
4	35	63.6	245	1	PHOS_FELICA	P16886_felis_silvestris	P16886 felis silvestris
5	35	63.6	246	1	PHOS_BAT	P20942_rattus_norvegicus	P20942 rattus norvegicus
6	35	63.6	340	1	CFAA_BSVEB	Q41729_bacillus_thuringiensis	Q41729 bacillus thuringiensis
7	35	63.6	424	1	VGLI_BSVEB	P18533_equus_hippicus	P18533 equine herpes
8	35	63.6	712	1	CDGT_BAC53	P09121_bacillus_sp	P09121 bacillus sp
9	35	63.6	713	1	AMYR_BAC58	P17692_bacillus_sp	P17692 bacillus sp
10	35	63.6	713	1	CDGT_BAC50	P05618_bacillus_sp	P05618 bacillus sp
11	35	63.6	713	1	CDGT_BAC5P	P30921_bacillus_sp	P30921 bacillus sp
12	35	63.6	713	1	CDGT_BAC51	P43379_bacillus_cereus	P43379 bacillus cereus
13	34	61.8	245	1	PHOS_CANFA	P07560_canis_familiaris	P07560 canis familiaris
14	34	61.8	246	1	PHOS_HUMAN	P20941_homo_sapiens	P20941 homo sapiens
15	34	61.8	345	1	ADH1_ASPEFL	P022749_aspergillus	P022749 aspergillus
16	34	61.8	349	1	ADH1_EMEMI	P08843_mericella	P08843 mericella
17	34	61.8	349	1	RADA_PYRFU	Q74036_pyrococcus	Q74036 pyrococcus
18	34	61.8	349	1	ADH3_EMEMI	P07754_mericella	P07754 mericella
19	34	61.8	352	1	ADH1_NEUCR	Q9p668_neurospora	Q9p668 neurospora
20	34	61.8	353	1	RADA_PYRFU	Q9v233_pyrococcus	Q9v233 pyrococcus
21	34	61.8	356	1	RADA_PYRFU	Q96001_pyrococcus	Q96001 pyrococcus
22	34	61.8	529	1	RADA_PYRFU	P54573_bacillus	P54573 bacillus
23	34	61.8	633	1	DXS_BAC5U	Q50739_streptomyces	Q50739 streptomyces
24	33	60.0	107	1	THIO_STRCL	P52230_streptomyces	P52230 streptomyces
25	33	60.0	110	1	ADHA_BHIME	Q31186_rhizobium	Q31186 rhizobium
26	33	60.0	340	1	CORT_DRONE	Q96033_drosophila	Q96033 drosophila
27	33	60.0	483	1	DOP2_DRONE	Q24563_drosophila	Q24563 drosophila
28	33	60.0	539	1	DOP2_DRONE	Q74708_lymnaea	Q74708 lymnaea
29	33	60.0	638	1	OAR1_LYMFST	P30920_bacillus	P30920 bacillus
30	33	60.0	718	1	CDGT_BAC51	P14014_bacillus	P14014 bacillus
31	33	60.0	718	1	CDGT_BAC55	P31747_bacillus	P31747 bacillus
32	33	60.0	718	1	CDGT_BAC55	Q15283_homo_sapiens	Q15283 homo sapiens

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1		INX4_DRONE		STANDARD;		PRF;		367 AA..			
AC	Q9YX6_drosophila	AC	Q9YX6	DT	16-OCT-2001 (Rel. 40, -created)	DT	16-OCT-2001 (Rel. 40, last sequence update)	DT	15-SEP-2003 (Rel. 42, last annotation update)		
DE	Innixin	DE	Innixin	GN	2PG OR INX4 OR CG10125.	GN	2PG OR INX4 (Innixin-1) (zero population growth protein).	GN	Drosophila melanogaster (Fruit fly).		
RA	Stubbings L.A., Todman M.G., Phillips R., Greer C.E., Tam J., Phelan P., Jacobs K., Bacon J.P., Davies J.A.,	RA	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila.	RA	PubMed-21953302; PubMed-11960713;	RA	Gap junctions in Drosophila: developmental expression of the entire Innixin gene family.	RA	[1]		
RL		RL		RN	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE TISSUE-Ovary.	RN	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE TISSUE-Ovary, AND DEVELOPMENTAL STAGE.	RN	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE TISSUE-Ovary, AND DEVELOPMENTAL STAGE.		
RA	Tazuke S.I., Schulz C., Gilboa L., Fogarty M., Mahowald A.P., Guichet A., Sphyrissi A., Wood C.G., Lehmann R., Fuller M.T., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.P., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Botkova D., Botchvar M.R., Bouck J., Brottier P., Burits K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dietz S.M., Dodin K., Douc L.B., Downes M., Dugan-Rocha S., Dunphy B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrera S., Perez C., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA	RA	PubMed-11973383;	RA	PubMed-11973383;	RA	PubMed-11973383;	RA	[2]		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutcliffe G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X., Amannatis P.G., Scherer S.E., Li P.W., Hostkins R.A., Galle R.M., Brandon R.C., Rogers Y.H.C., Blizquez R.G., Champe M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.P., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Development 129:2529-2539 (2002).	RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutcliffe G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X., Amannatis P.G., Scherer S.E., Li P.W., Hostkins R.A., Galle R.M., Brandon R.C., Rogers Y.H.C., Blizquez R.G., Champe M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.P., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Development 129:2529-2539 (2002).	RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutcliffe G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X., Amannatis P.G., Scherer S.E., Li P.W., Hostkins R.A., Galle R.M., Brandon R.C., Rogers Y.H.C., Blizquez R.G., Champe M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.P., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Development 129:2529-2539 (2002).	RA	[3]	RA	SEQUENCE FROM N.A., STRAIN=Berkeley;	RA	MEDLINE-20196006; PubMed-10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Sanger G., Sanger R., Ballew R.M., Bolshakov S., Bork P., Brottier P., Burton R.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dietz S.M., Dodin K., Douc L.B., Downes M., Dugan-Rocha S., Dunphy B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrera S., Perez C., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA	RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Sanger G., Sanger R., Ballew R.M., Bolshakov S., Bork P., Brottier P., Burton R.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dietz S.M., Dodin K., Douc L.B., Downes M., Dugan-Rocha S., Dunphy B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrera S., Perez C., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA	RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Sanger G., Sanger R., Ballew R.M., Bolshakov S., Bork P., Brottier P., Burton R.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dietz S.M., Dodin K., Douc L.B., Downes M., Dugan-Rocha S., Dunphy B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrera S., Perez C., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA	RA	[4]	RA	SEQUENCE FROM N.A., STRAIN=Berkeley;	RA	MEDLINE-20196006; PubMed-10731132;

Best Local Similarity		60.0%		Pred. No. 9.8;	
Matches		6		Conservative	
		1; Mismatches			
0					
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kravitz A.K., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon R., Nusskern D.R., Paclob J.M.,				
RA	Pallitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,				
RA	Shue B.C., Siden-Klaimos I., Simpson M., Skupski M.P., Smith T.,				
RA	Spier E., Spradling A.C., Stapleton C., Strong R., Sun E.,				
RA	Swanson R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,				
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,				
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,				
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,				
RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,				
RA	"The genome sequence of <i>Drosophila melanogaster</i> .";				
RA	Science 287:185-2195 (2000).				
[4]	SEQUENCE FROM N.A.				
RN	STRAIN=Berkeley; TISSUE=Embryo;				
RP	MEDLINE=22426066; PubMed=1237569;				
RC	RA				
RX	Stapleton M., Carlson J.W., Brookstein P., Yu C., Chambao M., Champenois M., Kromiller B., Paclob J.M., Park S., Wan K.H.,				
RA	George R.A., Guarin H., Kromiller B., Paclob J.M., Park S., Wan K.H.,				
RA	Rubin G.M., Celniker S.E.;				
RT	"A <i>Drosophila</i> full-length cDNA resource";				
RT	Genome Biol. 3:RESEARCH080.1-RESEARCH080.8(2002).				
RL	-1- FUNCTION: Structural component of the gap junctions in germ line cysts. Required for differentiation and survival of germ line cysts in females and of spermatogonia in males; gap junctional communication between spermatogonia and somatic cyst cells may be required for normal differentiation and survival of spermatogonia.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein; concentrated at the interface between germinal and somatic support cells in spermatogonia, early spermatocytes and germ cells in the ovary.				
CC	-1- TISSUE SPECIFICITY: Expressed in nurse cells and oocyte during oogenesis. Uniform expression in imaginal wing disk and low expression in developing imaginal CNS. Expressed in embryonic pole cells and primordial germ cells.				
CC	-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.				
CC	-1- SIMILARITY: Belongs to the innexin family.				
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CC	PRINTS: PB01242; INNEXIN				
CC	Gap Junction; Transmembrane.				
DR	KW	CYTOSMERIC (POTENTIAL).			
DR	FT DOMAIN	1	21		
DR	FT TRANSMEM	22	42	POTENTIAL.	
DR	FT DOMAIN	43	110	EXTRACELLULAR (POTENTIAL).	
DR	FT TRANSMEM	111	131	POTENTIAL.	
DR	FT DOMAIN	132	186	CYTOSMERIC (POTENTIAL).	
DR	FT TRANSMEM	187	207	POTENTIAL.	
DR	FT DOMAIN	208	268	EXTRACELLULAR (POTENTIAL).	
DR	FT TRANSMEM	269	289	POTENTIAL.	
DR	FT DOMAIN	290	367	CYTOSMERIC (POTENTIAL).	
DR	SEQUENCE	367 AA;	42784 MW;	B98A403DA7C3E CRC64;	
RA	65.5%; Score 36;	DB 1;	Length 367;		
RA	RESULT 3				
RA	PHOS_BOVIN				
ID	PROTEIN_BOVIN				
AC	P19632; P20940; Q28160;				
AC	P19632; P20940; Q28160;				
PRT;	245 AA;				

DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR PHOSducin (PDB) (33 kDa phototransducing protein) (MEKA protein).
 DR PF02114; Phosducin; 1.
 DR PRINTS; PR00677; PHOSDUCIN.
 DR Vision; Sensory transduction; Phosducin; 3D-structure.
 DR PHOSPHORYLATION (BY PKA).
 RW MOD-RES 73 73
 FT CONFLICT 44 44
 FT CONFLICT 238 239
 FT HELIX 21 35
 FT TURN 36 36
 FT HELIX 74 80
 FT TURN 81 82
 FT HELIX 87 105
 FT STRAND 114 116
 FT HELIX 120 128
 FT TURN 132 133
 FT STRAND 135 141
 FT TURN 143 144
 FT TURN 146 147
 FT HELIX 148 161
 FT TURN 163 164
 FT STRAND 166 171
 FT HELIX 172 175
 FT TURN 178 179
 FT STRAND 183 185
 FT TURN 188 193
 FT STRAND 194 195
 FT TURN 196 201
 FT TURN 202 203
 FT HELIX 204 207
 FT TURN 210 211
 FT HELIX 214 222
 FT TURN 223 225
 SQ SEQUENCE 245 AA; 28231 MW; SC621610401D550 CRC64;
 Query Match Score 63.6%; DB 1; Length 245;
 Best Local Similarity 87.5%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 TURVYKGG 10
 Db 188 TLYVYKGG 195

RESULT 4

PHOS_FELCA STANDARD; PRT; 245 AA.
 ID PA1686;
 AC P41686;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein).
 GN Felis silvestris catus (Cat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 CC NCBI_TaxID=9685;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=Abyssinian; TISSUE=Retina;
 RX MEDLINE-95178554; Published=7073608;
 RA Gorlin M.B., To A.C., Narfstrom K.;
 RT "Sequence analysis and exclusion of phosducin as the gene for the
 recessive retinal degeneration of the Abyssinian cat.";
 RL Biochim. Biophys. Acta 1260:323-327 (1995).
 CC -1- FUNCTION: MAY PARTICIPATE IN THE INTERACTION OF PHOTORECEPTOR
 PHOTOTRANSDUCTION OR IN THE INTERACTION OF VISUAL
 METABOLISM.
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
 CC the GTP-binding protein, transducin.
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
 CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
 CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
 CC -1- SIMILARITY: BELONGS TO THE PHOSducin FAMILY.
 CC -1- CATION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
 CC DUE TO A FRAMESHIFT.
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 CC or send an email to license@1sb.sib.ch).
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
 DR EMBL; M58170; AAA2716 1; -
 DR EMBL; M33529; AAA0349 1; -
 DR PIR; A38379; A38379.
 DR PDB; 1A0R; 16-FEB-99.
 DR InterPro; IPR001200; Phosducin.

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DR EMBL; L35214; AAB59257.1; -
 DR PIR; S52096; S52096.
 DR HSSP; P20942; 1B9X.
 DR InterPro; IPR001200; Phosducin.
 DR Pfam; PF02114; Phosducin_1.
 DR PRINTS; PRO0677; PHOSDUCIN.
 DR Vision; sensory transduction; Phosphorylation; PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 MOD_RES 73 73 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).

SEQUENCE 245 AA; 28363 MW; 9807CD30C32FFB21 CRC64;
 Score 35; DB 1; Length 245;
 Best Local Similarity 87.5%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Query 3 TLRYKGG 10
 | | | | | |
 Db 188 TLRYKGG 195

RESULT 5

PHOS_BAT
 ID PHOS_BAT STANDARD; PRT; 246 AA.
 AC P02942; 063420;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Phosducin (PBD) (33 kDa Phototransducing Protein) (MEKA Protein) (Rod photoreceptor 1) (RPR-1).
 GN PDC OR RPR1.
 OS Rattus norvegicus (Rod).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TAXID:10116; [1]

RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland, and Retina;
 RM MEDLINE=91007277; PubMed=21036181;
 RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
 RA Shinohara T.,
 RR Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
 retina and pineal gland.,
 RL Gene 91:209-215(1990).
 [2]

RN SEQUENCE FROM N.A.
 RC TISSUE=Pineal gland,
 RM MEDLINE=91301696; PubMed=2071146;
 RA Craft C.M., Lolley R.N., Seldin M.F., Lee R.H.;
 RR "Rat Pineal gland phosducin: cDNA isolation, nucleotide sequence, and
 chromosomal assignment in the mouse.";
 RL Genomics 10:400-409(1991),

RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH G-BETA AND G-GAMMA.
 RX MEDLINE=99288453; PubMed=10360181;
 RA Gaudet R., Savage J.R., McLaughlin J.N., Willardson B.M., Sigler P.B.;
 RR "A molecular mechanism for the phosphorylation-dependent regulation of heterotrimeric G-proteins by phosducin. Structural analysis of phosducin and its phosphorylation-regulated interaction with transducin beta-gamma.";
 RL Mol. Cell 3:649-660(1999).
 CC -I- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR METABOLISM.
 CC -I- SUBUNIT: forms a complex with the beta and gamma subunits of

CC the GTP-binding protein, transducin.
 CC -I- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
 CC -I- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
 CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
 CC -I- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
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 CC -I- DR EMBL; M33528; AAA0604 1; -
 CC -I- DR EMBL; M33530; AAA0603 1; -
 CC -I- DR EMBL; M60738; AAA41841 1; -
 CC -I- DR PIR; A39903; A39903.
 CC -I- DR JH0216; JH0216.
 CC -I- DR PDB; 1BX; 23-FEB-99.
 CC -I- DR PDB; 1BY; 23-FEB-99.
 CC -I- DR PDB; 2TRC; 05-JUN-97.
 CC -I- DR InterPro; IPRO01200; Phosducin.
 CC -I- DR InterPro; IPRO06653; Thioredoxin_dmd2.
 CC -I- DR Pfam; PF0211; Phosducin; 1.
 CC -I- DR PRNTS; PR00077; PHOSDUCIN.
 CC -I- KW Vision; Sensory transduction; Phosphorylation; 3D-structure.
 CC -I- FT MOD_RES 73 73 PHOSPHORYLATION (BY PKA).
 CC -I- FT VARIANT 191 191 V -> I.
 CC -I- FT CONFLICT 39 39 G -> S (IN REF. 2).
 CC -I- FT CONFLICT 88 88 G -> V (IN REF. 2).
 CC -I- FT CONFLICT 119 119 T -> S (IN REF. 2).
 CC -I- FT CONFLICT 211 211 D -> E (IN REF. 2).
 CC -I- FT TURN 37 37
 CC -I- FT HELIX 88 105
 CC -I- FT STRAND 114 116
 CC -I- FT TURN 120 120
 CC -I- FT HELIX 132 133
 CC -I- FT TURN 133 133
 CC -I- FT STRAND 135 141
 CC -I- FT TURN 143 144
 CC -I- FT TURN 146 147
 CC -I- FT HELIX 148 161
 CC -I- FT TURN 163 164
 CC -I- FT STRAND 166 171
 CC -I- FT HELIX 172 175
 CC -I- FT TURN 176 176
 CC -I- FT TURN 178 180
 CC -I- FT STRAND 183 185
 CC -I- FT TURN 188 193
 CC -I- FT STRAND 194 195
 CC -I- FT TURN 196 201
 CC -I- FT HELIX 204 207
 CC -I- FT HELIX 214 222
 CC -I- FT TURN 223 225
 CC -I- SQ SEQUENCE 246 AA; 28129 MW; 3C48ABCBA4E5B3D04 CRC64;
 CC -I- Query Match 63 6%; Score 35; DB 1; Length 246;
 CC -I- Best Local Similarity 87.5%; Pred. No. 10;
 CC -I- Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLRYKGG 10
 ID CFAA-BAC07
 AC 045729
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

RESULT 6
 CFAA-BAC07
 ID CFAA-BAC07
 AC 045729
 DT 188 TLRYKGG 195
 PRT; 340 AA.

DT 16-OCT-2001 (Rel.40, Last annotation update)
DE Pesticidial crystal protein cry15AA (Insecticidal delta-endotoxin
DE CRYXVAa) (Crystalline entomocidal protein) (38 kDa crystal
DE protein).
DE CRY15AA OR CRYXVA(A).
OS Bacillus thuringiensis (subsp. thompsoni).
OC Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=92105024; PubMed=1729243;
RA Brown F.L., Whittley H.R.;
RA "Molecular characterization of two novel crystal protein genes from
RA Bacillus thuringiensis subsp. thompsoni.";
RL Bacteriol. 174:549-557(1992).
CC -I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
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CC or send an email to license@ebi-sib.ch).
DR EMBL; M76442; AA022333.1; -
DR PIR; B41969; B41969.
DR InterPro; IPR005831; Aer_hem.
DR Toxin; Sporulation; Plasmid.
SQ SEQUENCE 340 AA; 37547 MW; BCBFA24FEB1FA50 CRC64;
Query Match 63.6%; Score 35; DB 1; Length 340;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Gaps 0; Indels 0;
Db 160 ATLQIYKG 9
Db 160 ATLQIYKG 167

RESULT 7
VGLL_HSVEB STANDARD; PRT; 424 AA.
AC P18553;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Glycoprotein I precursor.
GN OR 73.
OS Equine herpesvirus type 1 (strain Ab4P) (HSV-1), and
OS Equine herpesvirus type 1 (strain Ab1) (HSV-1), and
OS Equine herpesvirus type 1 (strain Kentucky D) (HSV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TAXID=31520; 10330;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=AB4P;
RX MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RA "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB1;
RA Kaneko T., Hamamoto T., Horikoshi K.;
RX MEDLINE=91276272; PubMed=1647359;
RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
RA Bonass W.A.;

RT "Sequence analysis of the 4.7-kb BamHI-ECORI fragment of the equine
DE herpesvirus type-1 short unique region.";
DE Gen 101:203-206(1991).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=Kentucky D;
RX MEDLINE=9110839; PubMed=2177089;
RA Audonet J.-C., Winslow J., Allen G., Paolletti E.;
RT "Equine herpesvirus type 1 unique short fragment encodes
RT glycoproteins with homology to herpes simplex virus type 1 gD, gI and
RT gE.";
RL J. Gen. Virol. 71:2969-2978(1990).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP19,
CC AND TO PRV GP63.
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CC EMBL; M86664; AA02508.1; -
DR EMBL; M36299; AAA66547.1; -
DR PIR; C36646; VGBEE9.
DR InterPro; IPR002874; Herpes_gI.
DR Pfam; PF01688; Herpes_gI; 1.
DR Glycoprotein; Signal; Transmembrane.
RN Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 424
FT DOMAIN 23 319
FT TRANSMEM 320 340
FT DOMAIN 341 424
FT CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 424 AA; 46392 MW; B99BEE7/DA895806 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 424;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
CDGT_BAC53 STANDARD;
ID CDGT_BAC53
AC P09121;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cyclomaltoextrin glucanoctransferase precursor (EC 2.4.1.19)
DE (Cycloextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 38-2).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TAXID=1412;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-44.
RX MEDLINE=89036108; PubMed=2972812;
RA Kaneko T., Hamamoto T., Horikoshi K.;
RX "Molecular cloning and nucleotide sequence of the cyclomaltoextrin
RT glucanotransferase gene from the alkalophilic Bacillus sp. strain no.
RA 38-2.";

RL J. Gen. Microbiol. 134:97-105(1988).
 RN [2] SEQUENCE OF 1-386 FROM N.A.
 RP Hamamoto T., Kaneko T., Horikoshi K.;
 RA Nucleotide sequence of the cyclomaltohexaextrin glucanotransferase
 RR (CGTase) gene from alkaliphilic *Bacillus* sp. strain No. 38-2.;
 RL Agric. Biol. Chem. 51:2019-2022(1987).
 -I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -I- COFACTOR: BINDS TWO CALCIUM IONS.
 CC -I- SUBSTRATE: Maltodextrin.
 CC -I- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTRUCTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC
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 CC
 DR M19880: AAA22309_1; -
 DR EMBL: D00129; BAA00077_1; -
 DR HSSP: P05618; IPIAM.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006048; Alpha_amyl_C.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR002044; CBD_4.
 DR InterPro: IPR002309_1; -
 DR PRODOM: IPR005909; IPT_TIG.
 DR Pfam: PF00128; alpha_amylase_1.
 DR Pfam: PF02806; alpha_amylase_C; 1.
 DR Pfam: PF00686; Alpha_amyl_1_C.
 DR Pfam: PF01833; TIG; 1.
 DR PRINTS; PRO0110; ALPHAAMYLASE.
 DR SMART; SM00642; Amyl; 1.
 DR SMART; SM00632; Amyl_C; 1.
 DR SIGNAL; Glycosyltransferase; Calcium; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 712 CYCLONALTODEXTRIN GLUCANOTRANSFERASE.
 FT DOMAIN 28 165 A1.
 FT DOMAIN 166 229 B.
 FT DOMAIN 230 433 A2.
 FT DOMAIN 434 522 C.
 FT DOMAIN 523 608 D.
 FT DOMAIN 609 712 E.
 FT DISULFID 707 77 BY SIMILARITY.
 FT ACT_SITE 256 256 BY SIMILARITY.
 FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT CONFLICT 582 586 VPGGI -> SVRHL (IN REF. 2).
 SQ SEQUENCE 712 AA; 78249 MW; 4F0A8F70BEF81B99 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 712;
 Best Local Similarity 60.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATALRYKGG 10
 ID AMYR_BAC58 STANDARD; PRT; 713 AA.
 Db 70 CTNLRVYCGG 79

AC P17692;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Nucleic acid-digesting amylase precursor (EC 3.2.1.1) (1,4-alpha-D-
 DE glucan glucanohydrolase).
 DE *Bacillus* sp. (strain B1018).
 OS *Bacillus*; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OC
 OX NCBI_TaxID=1417;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=90147765; PUBMED=1689153;
 RA Itkor P., Tsutagoshi N., Ueda S.;
 RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
 RT *Bacillus* sp. B1018 and its strong homology to the cyclodextrin
 RT glucanotransferase genes";
 RL Biochem. Biophys. Res. Commun. 166:630-636 (1990).
 CC -I- FUNCTION: THIS ENDO-TYPE ADSORBABLE AMYLASE IS CAPABLE TO
 CC DIGEST RAW STARCH.
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC
 DR EMBL: M33102; AAA22339_1; -
 DR EMBL; D90112; BAA14140_1; -
 DR PIR; S09196; S09196.
 DR HSSP; P43379; ICDG.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam: PF00128; alpha_amylase; 1.
 DR Pfam; PF02806; Glycosyltransferase; Calcium; Signal.
 DR Pfam; PF00686; Alpha_amyl_1_C.
 DR Pfam; PF00686; CBD_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRINTS; PRO0110; ALPHAAMYLASE.
 DR PRODOM; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amyl; 1.
 DR SMART; SM00632; Amyl_C; 1.
 DR SIGNAL; Glycosyltransferase; Calcium; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713 RAW-STARCH-DIGESTING AMYLASE.
 FT ACT_SITE 256 256 BY SIMILARITY.
 FT ACT_SITE 260 260 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT SEQUENCE 713 AA; 77442 MW; 85FF616D687B988 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 713;
 Best Local Similarity 60.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATALRYKGG 10
 ID CDT_BAC50 STANDARD; PRT; 713 AA.
 Db 70 CTNLRVYCGG 79

RESULT 10
 CDT_BAC50
 ID CDT_BAC50 STANDARD; PRT; 713 AA.
 AC P05618;

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
 RX MEDLINE=9025759; PubMed=2534500;
 RA Kaneko T.; Song K.B.; Hamamoto T.; Kudo T.; Horikoshi K.;
 RT Construction of a chimeric series of *Bacillus* cyclomaltotetraextrin ph
 RT glucoamylotransferases and analysis of the thermal stabilities and pH
 RT optima of the enzymes.;
 RL J. Gen. Microbiol. 135:3447-3457 (1989);
 CC -I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -I- COFACTOR: Binds two calcium ions.
 CC -I- SUBSTRATE: Monomer.
 CC -I- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,6-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOGLYOSACCHARIDE PRODUCED.
 CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC
 EMBL; M28053; AAA22310; 1; -.
 DR HSSP; P43379; ICDG.
 DR InterPro; IPR005589; Alpha_amyl_cat_sub.
 DR InterPro; IPR006048; Alpha_amy_C.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR003044; CBD_4.
 DR InterPro; IPR003909; IPT_TIG.
 DR Pfam; PF00128; alpha_amylase_1.
 DR Pfam; PF02806; Alpha_amylase_C_1.
 DR Pfam; PF00686; CBM_20_1.
 DR Pfam; PF01833; TIG_1.
 DR ProDom; P0001568; CBD_4_1.
 DR SMART; SM00632; Amy_1.
 DR Transierase; Glycosyltransferase; Calcium; Signal.
 KW CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
 FT SIGNAL 1 27
 FT CHAIN 28 713
 FT DOMAIN 28 165
 FT DOMAIN 166 229
 FT DOMAIN 230 433
 FT DOMAIN 434 522
 FT DOMAIN 523 609
 FT DOMAIN 610 713
 FT DISULFID 70 77
 FT ACT_SITE 256 256
 FT ACT_SITE 284 284
 FT ACT_SITE 355 355
 SQ SEQUENCE 713 AA; 77389 MW; D13AEF6C507FF45E CRC64;
 Query Match 63.68; Score 35; DB 1; Length 713;
 Best Local Similarity 60.04; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CATALRYKGG 10
 | | | | | | | |
 Db 70 CTNLRLYCGG 79
 RESULT 11
 CDBT_BACSP STANDARD; PRT; 713 AA.
 ID CDBT_BACSP STANDARD; PRT; 713 AA.
 AC P30921;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Cyclomaltotetraextrin glucoamylotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase).
 GN Bacillus sp. (strain 17-1)
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
 OC NCBI_TAXID=1409;
 RN [1]

Query Match 63.68; Score 35; DB 1; Length 713;
 Best Local Similarity 60.04; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CATALRYKGG 10
 | | | | | | | |
 Db 70 CTNLRLYCGG 79
 RESULT 12
 CDDG_BACCI STANDARD; PRT; 713 AA.
 ID CDDG_BACCI STANDARD; PRT; 713 AA.
 AC P43379;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin glycosyltransferase) (CGTase).
 OS *Bacillus circulans*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TAXID:1397;
 RN [1] RP SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP STRAIN="251";
 RX MEDLINE=94149761; PubMed=8107143;
 RA Lawson C.L., van Montfort R., Strokopystov B., Rozeboom H.J.,
 RA Kalk K.H., de Vries G.E., Pennings D., Dijkhuizen L., Dijkstra B.W.;
 RT "Nucleotide sequence and X-ray structure of cyclodextrin
 RT glycosyltransferase from *Bacillus circulans* strain 251 in a maltose-
 RT dependent crystal form";
 RL J. Mol. Biol. 236:590-600(1994).
 RN [2] RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC STRAIN="251";
 RX MEDLINE=6094317; PubMed=7493956;
 RA Knegtel R.M.A., Strokopystov B., Pennings D., Faber O.G.,
 RA Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
 RT "Crystallographic studies of the interaction of cyclodextrin
 RT glycosyltransferase from *Bacillus circulans* strain 251 with natural
 RT substrates and products";
 RL J. Biol. Chem. 270:29256-29264(1995).
 RN [3] RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=97115811; PubMed=8951113;
 RA Pennings D., van der Veen B.A., Knegtel R.M., van Hijum S.A.,
 RA Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
 RT "The raw starch binding domain of cyclodextrin glycosyltransferase
 RT from *Bacillus circulans* strain 251";
 RL J. Biol. Chem. 271:32777-32784(1996).
 RN [4] RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
 RC STRAIN="251";
 RX MEDLINE=96264806; PubMed=8672460;
 RA Strokopystov B., Knegtel R.M.A., Pennings D., Rozeboom H.J., Kalk K.H.,
 RA Dijkhuizen L., Dijkstra B.W.;
 RT "Structure of cyclodextrin glycosyltransferase complexed with a
 RT maltosonase inhibitor at 2.6-A resolution. Implications for product
 RT specificity";
 RL Biochemistry 35:1241-1249(1996).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds two calcium ions.
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: May consist of two protein domains: the one in the amino-
 CC terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
 CC the other in the C-terminal side catalyzes other activities,
 CC including the reconstitution of an alpha-1,4-glucosidic linkage
 CC for cyclizing the maltooligosaccharide produced.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSTYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC
 DR EMBL; X78145; CAA55023.1; -
 DR PIR; A58800; A58800.
 DR PDB; 20CG; 14-OCT-98.
 DR PDB; 1CDG; 08-MAR-95.
 DR PDB; 1CGV; 27-FEB-95.
 DR PDB; 1CGW; 27-FEB-95.
 DR PDB; 1CGX; 07-FEB-95.
 DR PDB; 1CGY; 07-FEB-95.
 DR PDB; 1CME; 15-DEC-95.

DR PDB; 1CME; 15-DEC-95.
 DR PDB; 1CME; 15-DEC-95.
 DR PDB; 1CME; 15-DEC-95.
 DR PDB; 2D1J; 13-JAN-99.
 DR PDB; 1RCM; 21-APR-97.
 DR PDB; 1CME; 07-FEB-00.
 DR PDB; 1CML; 03-SEP-99.
 DR PDB; 1D3C; 22-DEC-99.
 DR PDB; 1DNU; 06-MAR-00.
 DR 1B05; 22-NOV-00.
 DR 1B07; 22-NOV-00.
 DR 1CKK; 16-JAN-02.
 DR InterPro; 1P006389; Alpha_amyl_cat_sub.
 DR InterPro; 1P006048; Alpha_amyl_C.
 DR InterPro; 1P006047; Alpha_amyl_cat.
 DR InterPro; 1P002044; CBD_4.
 DR InterPro; 1P006046; Glyco_hydro_13.
 DR InterPro; 1P002919; IPT_TIG.
 DR Pfam; PF00128; alpha-amylase_1.
 DR Pfam; PF02806; alpha-amylase_C; 1.
 DR Pfam; PF00688; CBD_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRIMTS; PRO00110; ALPHAAMYLASE.
 DR ProdDom; PD000568; CBD_4; 1.
 DR SMART; SM00542; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 KW Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
 FT SIGNAL; 1
 FT CHAIN; 27
 FT DOMAIN; 1
 FT DOMAIN; 28
 FT DOMAIN; 28
 FT DOMAIN; 229
 FT DOMAIN; 433
 FT DOMAIN; 230
 FT DOMAIN; 522
 FT DOMAIN; 523
 FT DOMAIN; 609
 FT DOMAIN; 610
 FT DOMAIN; 713
 FT DISULFID; 70
 FT ACT_SITE; 256
 FT ACT_SITE; 284
 FT ACT_SITE; 355
 FT TURN; 31
 FT TURN; 30
 FT TURN; 33
 FT TURN; 34
 FT TURN; 36
 FT TURN; 40
 FT SPAND; 44
 FT SPAND; 45
 FT SPAND; 49
 FT SPAND; 52
 FT SPAND; 57
 FT SPAND; 59
 FT SPAND; 63
 FT SPAND; 65
 FT SPAND; 66
 FT SPAND; 69
 FT SPAND; 73
 FT SPAND; 74
 FT SPAND; 76
 FT SPAND; 76
 FT SPAND; 81
 FT SPAND; 89
 FT SPAND; 90
 FT SPAND; 91
 FT SPAND; 92
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 FT SPAND; 154
 FT SPAND; 155
 FT SPAND; 156
 FT SPAND; 163
 FT SPAND; 167
 FT SPAND; 170
 FT SPAND; 173
 FT SPAND; 174
 FT SPAND; 176
 FT SPAND; 177
 FT SPAND; 179
 FT SPAND; 182
 FT SPAND; 184

Qy	1	CATLRYKGG	10
db	70	CTNRLIGGG	79

RESULT 13

PHOS_CANFA_ID	PHOS_CANFA	STANDARD;	PRT;	245 AA.
075560;	AC	15-JUL-1999 (Rel. 38, Created)	DT	15-JUL-1999 (Rel. 38, Last sequence update)
	AC	28-FEB-2003 (Rel. 41, Last annotation update)	DT	Phosducin (PHD) (33 kDa phototransducing protein).
	AC	PDC.	GN	Canis familiaris (Dog).
	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	OC	
	OC		NCBI_TAXID=9615;	
	OC		[1]	
	RN			

SEQUENCE FROM N.A., AND VARIANT PD GLY-82.
 MEDLINE-#98382516; PubMed-9714819;
 Zhang Q., Aciland G.M., Parshall C.J., Hask
 Aguirre G.D.;
 "Characterization of canine photoreceptor
 identification of a sequence variant in do
 RT dysplasia.",
 RT
 Gene 215:231-239(1998).
 -1- FUNCTION: MAY PARTICIPATE IN THE REGUL
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATIO
 CC METABOLISM.
 CC -1- SUBUNIT: Forms a complex with the beta
 CC -1- GTP-binding protein, transducin.
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER
 CC (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN PDC ARE THE CAUSE
 CC (PD); AN AUTOSOMAL RECESSIVE DISEASE O
 CC CAUSING RETINAL DEGENERATION.
 CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN F
 CC
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 EMBL: AF066874; AAC72749.1; -.
 DR HSSP; P2094; 1B9X.
 DR InterPro; IPR01200; Phosducin.
 DR InterPro; IPR006663; Thioredoxin_dom2.
 DR pfam; PF02114; Phosducin_1.
 DR PRINTS; PRO0677; PRODUCIN.
 FT Vision: Sensory transduction; Phosphorylat
 FT NOD_RRS 73 73 PHOSPHORYLAT
 FT VARIANT 82 82 R > G (IN PD
 SQ SEQUENCE 245 AA; 28263 MW; CFA3779E2B7

Query Match Score 34; DB
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1

Qy 3 TLRYKGG 10
 db 188 TLRYKGG 195

RESULT 14
 PHOS_HUMAN
 ID PHOS_HUMAN STANDARD; PRT; 246 A
 AC P20941; Q14816;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing p
 GN PDC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Ve
 OC Mammalia; Eutheria; Primates; Catarrhini;
 OX NCBI_Taxid:9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Pinéal gland, and Retina;
 MEDLINE-#91007277; PubMed-221081;
 RA Abe T., Nakabayashi H., Tamada H., Takagi
 RA Shinohara T.;
 RT "Analysis of the human, bovine and rat 33-
 RT retinal and pineal gland.",
 RL Gene 91:209-215(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-#90343823; PubMed-2383274;
 RP SEQUENCE FROM N.A.
 RX MEDLINE-#90343823; PubMed-2383274;

RT "Complete amino acid sequence of human plasma beta 2-glycoprotein I.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
 RN [9].
 RP SEQUENCE OF 20-38.
 RC TISSUE/FOLLICULAR fluid;
 RX MEDLINE-2148138; PubMed-11250549;
 RA Aleporou-Marinou V., Pappa H., Yalouris P., Patargas T.;
 RT "Purification of apolipoprotein H (beta 2-glycoprotein I)-like protein
 from human follicular fluid.";
 RL Comp. Biochem. Physiol. 128B:537-542(2001).
 RN [10].
 RP DISULFIDE BONDS IN C-TERMINAL DOMAIN.
 RX MEDLINE-9305249; PubMed-1426288;
 RA Steinbässerer A., Barlow P.N., Willis A.C., Kertesz Z.,
 RA Campbell I.D., Sim R.B., Norman D.G.;
 RT "Activity, disulphide mapping and structural modelling of the fifth
 domain of human beta 2-glycoprotein I.;"
 RL FEBS Lett. 313:193-197(1992).
 RN [11].
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE-9729944; PubMed-9155091;
 RA Gambino R., Ruiu G., Pagano G., Cassader M.;
 RT "Qualitative analysis of the carbohydrate composition of
 apolipoprotein H.";
 RL J. Protein Chem. 16:205-212(1997).
 RN [12].
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX TISSUE/Plasma;
 RX MEDLINE-99437994; PubMed-10508150;
 RA Bouma B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G.,
 RA Schouten A., Smulders M.J.A., Derkx R.H.W.M., Kroon J., Gros P.;
 RT "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids
 based on its crystal structure.";
 RL EMBO J. 18:5166-5174(1999).
 RN [13].
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE-9031634; PubMed-1056355;
 RA Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M.,
 RA Lagger P., Prassl R.;
 RT "Crystal structure of human beta2-glycoprotein I: implications for
 protein-lipid binding and the antiphospholipid syndrome.";
 RL EMBO J. 18:6228-6239(1999).
 RN [14].
 RP VARIANT LEP-266.
 RX MEDLINE-93273313; PubMed-8099061;
 RA Steinbässerer A., Doerner C., Wuerzner R., Sim R.B.;
 RT "Human beta 2-glycoprotein I: molecular analysis of DNA and amino
 acid polymorphism.";
 RL Hum. Genet. 91:401-402(1993).
 RN [15].
 RP VARIANT ASN-107.
 RX MEDLINE-9736941; PubMed-9225959;
 RA Sanghera D.K., Kristoffersen T.; Hammann R.F., Kamboh M.I.;
 RT "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I)
 protein polymorphism.";
 RL Hum. Genet. 100:57-62(1997).
 RN [16].
 RP VARIANTS GSX-325 AND SER-335.
 RX MEDLINE-97217791; PubMed-9063752;
 RA Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;
 RT "Identification of structural mutations in the fifth domain of
 apolipoprotein H (beta-2-glycoprotein I) which affect phospholipid
 binding.";
 RL Hum. Mol. Genet. 6:311-316(1997).
 RC - FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
 CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC - SIMILARITY: Contains 4 Sushi (SCR) domains.

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 DR EMBL; X58100; CAA41113.1;
 DR EMBL; X53555; CAA37664.1;
 DR EMBL; X57847; CAA40977.1;
 DR EMBL; X57176; AAA51766.1;
 DR EMBL; M62839; AAA51766.1;
 DR EMBL; S80305; AAB21330.1;
 DR EMBL; Y11493; CAA72219.1;
 DR EMBL; Y11494; CAA72219.1;
 DR EMBL; Y11495; CAA72219.1;
 DR EMBL; X53595; CAA72219.1;
 DR EMBL; Y11496; CAA72219.1;
 DR EMBL; Y11497; CAA72219.1;
 DR EMBL; Y11498; CAA72219.1;
 DR EMBL; Y17754; CAA76845.1;
 DR EMBL; BC020703; AAH20703.1;
 DR EMBL; BC056283; AAH6283.1;
 DR PIR; S17178; NBNU.
 DR IQUB; 08-OCT-99.
 DR ICB; 19-NOV-99.
 DR PDB; 1G4F; 28-MAR-01.
 DR PDB; 1G4G; 28-MAR-01.
 DR Genew/HGNC:616; APOH.
 DR MIM; 138700;
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00084; sushi_4.
 DR SMART; SM00032; CCP_4.
 DR Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal;
 DR Polymorphism; 3D-structure.
 FT SIGNAL 1 19 BETA-2-GLYCOPROTEIN I.
 FT CHAIN 20 345 SUSHI 1.
 FT DOMAIN 22 80
 Query Match Score 34; DB 1; Length 345;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 2 ATLVYK 8
 FT 111111
 Db 151 ATLVYK 157
 Search completed: August 28, 2003, 18:35:08
 Job time : 6.15152 secs

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